

REMARKS**INTRODUCTION:**

In accordance with the foregoing, claims 5-11 and 21 have been amended, and claims 25-27 have been added. No new matter is being presented, and approval and entry are respectfully requested.

Claims 5-11, 21, 24 and 25-27 are pending and under consideration. Reconsideration is respectfully requested.

REJECTION UNDER 35 U.S.C. §101:

In the Office Action, at pages 2-7, claims 5-11, 21 and 24 were rejected under 35 U.S.C. §101 for the reasons set forth therein. This rejection is traversed and reconsideration is requested.

Claims 5-11 and 24 were rejected as being directed to non-statutory subject matter.

Independent claims 5 and 21 have been amended to recite more specifically that the present claimed invention discloses a method and an apparatus for analyzing three-dimensional structures of a predetermined amino acid sequence probe and a protein molecule target, wherein the predetermined amino acid sequence includes a first structure expressed by three-dimensional coordinates of elements belonging to a first point set and the protein molecule target includes a second structure expressed by three-dimensional coordinates of elements belonging to a second point set, to determine a degree of similarity between the three dimensional structure of the predetermined amino acid sequence probe represented by the three-dimensional coordinates of the elements belonging to the first point set and the three-dimensional structure of the protein molecule target represented by the three-dimensional coordinates of elements belonging to the second point set.

Thus, claims 5 and 21 produce a practical application that is directed to statutory subject matter, has utility and has a concrete, tangible and useful result. Hence, claims 5 and 21 are submitted to be in allowable form under 35 U.S.C. §101. Since claims 6-11 and 24 depend, directly or indirectly, from amended claim 5, claims 6-11 and 24 are submitted to be in allowable form under 35 U.S.C. §101 for at least the reasons that amended claim 5 is submitted to be in allowable form under 35 U.S.C. §101.

REJECTION UNDER 35 U.S.C. §112:

In the Office Action, at pages 7-10, claims 5-11, 21 and 24 were rejected under

35 U.S.C. §112, first paragraph, for the reasons set forth therein. This rejection is traversed and reconsideration is requested.

The terminology “at least one of” has been cancelled. Thus, the claims containing same are now submitted to be clear under 35 U.S.C. §112, first paragraph.

The Examiner submits that claims 5-11 21 and 24 fail to comply with the enablement requirement. However, it is respectfully submitted that paragraph [0162] of the published application recites; “Accordingly, in generating correspondence between these sets, it is designed to generate a desired combination in view of the geometric relationship within the respective sets, the threshold value condition, and the attribute of points described in detail in (4), (5), (6) below.”

(4) is described in paragraphs [0178]-[[0190]. (5) is described in paragraphs [0191]-[0197]. (6) is described in paragraphs [0198]-[0201]. It is respectfully submitted that (4)-(6) are clear to one skilled in the art, and that (4)-(6) set forth clearly how to generate a desired combination. The desired combinations obtained are then compared, based on minimizing the root mean square distance (rmsd) values, and a one having a lowest rmsd is selected - see paragraph [0173]). For example, a permissible error range of 0.5 is selected in FIGs. 19A-19B, and point b_p is selected because it is within the permissible error range. Hence, the optimum combination has been renamed “desired combination” and has been clarified by explaining more clearly that said desired combination is based on a predetermined minimized geometric distance. Paragraph [0205] describes criteria for determining attributes of a point and has been incorporated into the independent claims. Section (5) explains the use of a predetermined threshold value, which has been clarified by the amendment of the independent claims. It is respectfully submitted that it is clear to one skilled in the art how to combine the selection of a minimized rmsd, the comparison of the attributes and the determination of whether a predetermined threshold value has been reached to provide an optimal combination. The terminology “in view of” has been deleted. The amendment of the independent claims is submitted to describe the generation of comparisons and the determination of whether the requirements have been met.

Thus, it is respectfully submitted that amended independent claims 5 and 21 comply with the written description requirement and are enabling under 35 U.S.C. §112, first paragraph. Since claims 6-11 and 24 depend from amended claim 5, claims 6-11 and 24 are submitted to comply with the written description requirement and to be enabling under 35 U.S.C. §112, first paragraph, for at least the reasons that amended claim 5 is submitted to comply with the written

description requirement and to be enabling under 35 U.S.C. §112, first paragraph.

NEW CLAIMS:

New claim 25 recites that the features of the present invention include a method of analyzing three-dimensional structures of a predetermined molecular structure probe and a molecular structure target, wherein the predetermined molecular structure probe includes a first structure expressed by three-dimensional coordinates of elements belonging to a first point set and the molecular structure target includes a second structure expressed by three-dimensional coordinates of elements belonging to a second point set, to determine a degree of similarity between the three dimensional structure of the predetermined molecular structure probe represented by the three-dimensional coordinates of the elements belonging to the first point set and the three-dimensional structure of the molecular structure target represented by the three-dimensional coordinates of elements belonging to the second point set, comprising: generating, by a superposition calculating unit, a combination of correspondence satisfying a condition between the elements belonging to the first point set and the elements belonging to the second point set from among all candidates for the combination of correspondence, wherein the condition includes generating a desired combination based on a predetermined minimized geometric distance between the first and second point sets, setting a predetermined threshold value and pruning a retrieval path if an attribute value of a candidate is greater than the predetermined threshold value, and determining that a point is a candidate if an attribute of an element of the first point set includes a type of an atom, an atomic group, and a molecule, a hydrophilic property, a hydrophobic property, or a positive or negative charge that coincides with an attribute of an element of the first point set, and refining the elements of the first and second point sets based on an attribute of the elements of the first and second point sets; calculating, by the superposition calculating unit, a root mean square distance between the elements belonging to the first point set relating to the elements belonging to the second point set in the generated combination of correspondence; determining, by the superposition calculating unit, based on the generated combination of correspondence and minimizing root mean square distance values, similar portions of the three dimensional structure of the predetermined molecular structure probe represented by the three-dimensional coordinates of the elements belonging to the first point set and the three-dimensional structure of the molecular structure target represented by the three-dimensional coordinates of elements belonging to the second point set; and displaying, by a graphic display unit, the three-dimensional structures of the predetermined molecular structure probe and the molecular structure target in an overlapped manner based on the

generated combination of correspondence and minimized root mean square distance values, wherein the first and second point sets, respectively, are sequence listings defining the predetermined molecular structure probe and the molecular structure target, respectively.

New claim 25 is supported by paragraphs [0202] and [0214].

Nothing in the prior art teaches or suggests such. It is submitted that new claim 25 distinguishes over the prior art.

New claim 26 recites that the features of the present invention include a computer-readable medium containing computer-readable instructions to analyze three-dimensional structures of a predetermined molecular structure probe and a molecular structure target, wherein the predetermined molecular structure probe includes a first structure expressed by three-dimensional coordinates of elements belonging to a first point set and the molecular structure target includes a second structure expressed by three-dimensional coordinates of elements belonging to a second point set, to determine a degree of similarity between the three dimensional structure of the predetermined molecular structure probe represented by the three-dimensional coordinates of the elements belonging to the first point set and the three-dimensional structure of the molecular structure target represented by the three-dimensional coordinates of elements belonging to the second point set, the computer-readable instructions comprising: generating a combination of correspondence satisfying a condition between the elements belonging to the first point set and the elements belonging to the second point set from among all candidates for the combination of correspondence, wherein the condition includes generating a desired combination based on a predetermined minimized geometric distance between the first and second point sets, setting a predetermined threshold value and pruning a retrieval path if an attribute value of a candidate is greater than the predetermined threshold value, and determining that a point is a candidate if an attribute of an element of the first point set includes a type of an atom, an atomic group, and a molecule, a hydrophilic property, a hydrophobic property, or a positive or negative charge that coincides with an attribute of an element of the first point set, and refining the elements of the first and second point sets based on an attribute of the elements of the first and second point sets; calculating, by the superposition calculating unit, a root mean square distance between the elements belonging to the first point set relating to the elements belonging to the second point set in the generated combination of correspondence; determining, based on the generated combination of correspondence and minimizing root mean square distance values, similar portions of the three dimensional structure of the predetermined molecular structure probe represented by the three-dimensional coordinates of the elements belonging to the first point set and the three-

dimensional structure of the molecular structure target represented by the three-dimensional coordinates of elements belonging to the second point set; and causing to be displayed, on a display, the three-dimensional structures of the predetermined molecular structure probe and the molecular structure target in an overlapped manner based on the generated combination of correspondence and minimized root mean square distance values, wherein the first and second point sets, respectively, are sequence listings defining the predetermined molecular structure probe and the molecular structure target, respectively.

New claim 26 is supported by paragraphs [0022]-[0023], i.e., automation is achieved via programming the operations.

Nothing in the prior art teaches or suggests such. It is submitted that new claim 26 distinguishes over the prior art.

New claim 27 recites that the features of the present invention include an apparatus for analyzing three-dimensional structures of a predetermined molecular structure probe and a molecular structure target, wherein the predetermined molecular structure probe includes a first structure expressed by three-dimensional coordinates of elements belonging to a first point set and the molecular structure target includes a second structure expressed by three-dimensional coordinates of elements belonging to a second point set, to determine a degree of similarity between the three dimensional structure of the predetermined molecular structure probe represented by the three-dimensional coordinates of the elements belonging to the first point set and the three-dimensional structure of the molecular structure target represented by the three-dimensional coordinates of elements belonging to the second point set, comprising: a database having data having stored therein that includes a plurality of three-dimensional molecular structures of substances representing a plurality of predetermined molecular structure probes, each having a first structure expressed by three-dimensional coordinates of elements belonging to a first point set; a data input unit that reads the data and an input command from a user selecting a molecular structure target that includes the second structure expressed by three-dimensional coordinates of elements belonging to the second point set; a superposition calculation unit that generates a combination of correspondence satisfying a condition between the elements belonging to the first point set and the elements belonging to the second point set from among all candidates for the combination of correspondence, wherein the condition includes generating a desired combination based on a predetermined minimized geometric distance between the first and second point sets, setting a predetermined threshold value and pruning a retrieval path if an attribute value of a candidate is greater than the predetermined threshold value, and determining that a point is a candidate if an attribute of an element of the

first point set includes a type of an atom, an atomic group, and a molecule, a hydrophilic property, a hydrophobic property, or a positive or negative charge that coincides with an attribute of an element of the first point set, determines a degree of similarity between the three-dimensional structure of the predetermined molecular structure probe represented by the three-dimensional coordinates of the elements belonging to the first point set and the three-dimensional structure of the molecular structure target represented by the three-dimensional coordinates of elements belonging to the second point set, and superposes a three-dimensional molecular structure of a predetermined molecular structure probe read from the database with a three-dimensional molecular structure target in accordance with the desired combination and having minimized root mean square distance values; and a graphic display unit that displays the three-dimensional structures of the predetermined molecular structure probe and the molecular structure target in an overlapped manner based on the calculations of the superposition calculation unit.

New claim 27 is supported by FIG. 22 and paragraph [0205].

Nothing in the prior art teaches or suggests such. It is submitted that new claim 27 distinguishes over the prior art.

CONCLUSION:

In accordance with the foregoing, it is respectfully submitted that all outstanding objections and rejections have been overcome and/or rendered moot, and further, that all pending claims patentably distinguish over the prior art. Thus, there being no further outstanding objections or rejections, the application is submitted as being in condition for allowance which action is earnestly solicited.

If the Examiner has any remaining issues to be addressed, it is believed that prosecution can be expedited by the Examiner contacting the undersigned attorney for a telephone interview to discuss resolution of such issues.

If there are any underpayments or overpayments of fees associated with the filing of this Amendment, please charge and/or credit the same to our Deposit Account No. 19-3935.

Respectfully submitted,

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